Neutrokine-α

```
   1  AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC  60

  61  ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC  120

 121  CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC  180
   1                              M  D  D  S  T  E  R  E  Q  S  R  L   12

 181  TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC  240
  13    T  S  C  L  K  K  R  E  E  M  K  L  K  E  C  V  S  I  L  P   32
                                                                CD-I

 241  CACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT  300
  33    R  K  E  S  P  S  V  R  S  S  K  D  G  K  L  L  A  A  T  L   52
                     CD-I

 301  TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCC  360
  53    L  L  A  L  L  S  C  C  L  T  V  V  S  F  Y  Q  V  A  A  L   72

 361  TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC  420
  73    Q  G  D  L  A  S  L  R  A  E  L  Q  G  H  H  A  E  K  L  P   92
                     CD-II

 421  CAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC  480
  93    A  G  A  G  A  P  K  A  G  L  E  E  A  P  A  V  T  A  G  L  112
                     CD-III
                                    #
 481  TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA  540
 113    K  I  F  E  P  P  A  P  G  E  G  N  S  S  Q  N  S  R  N  K  132

 541  AGCGTGCCGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG  600
 133    R  A  V  Q  G  P  E  E  T  V  T  Q  D  C  L  Q  L  I  A  D  152
                                                          CD-IV
```

FIG. 1A

Neutrokine-α

```
601  ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT  660
153    S  E  T  P  T  I  Q  K  G  S  Y  T  F  V  P  W  L  L  S  F  172
                                                 CD-V

661  TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTT  720
173    K  R  G  S  A  L  E  E  K  E  N  K  I  L  V  K  E  T  G  Y  192
          CD-V                                    CD-VI

721  ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA  780
193    F  F  I  Y  G  Q  V  L  Y  T  D  K  T  Y  A  M  G  H  L  I  212
                      CD-VI                          CD-VII

781  TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT  840
213    Q  R  K  K  V  H  V  F  G  D  E  L  S  L  V  T  L  F  R  C  232
             CD-VII                                 CD-VIII

                              #
841  GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAA  900
233    I  Q  N  M  P  E  T  L  P  N  N  S  C  Y  S  A  G  I  A  K  252
          CD-VIII                              CD-IX

901  AACTGGAAGAAGGAGATGAACTCCAACTTGCAATACCAAGAGAAAATGCACAAATATCAC  960
253    L  E  E  G  D  E  L  Q  L  A  I  P  R  E  N  A  Q  I  S  L  272
                      CD-X

961  TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT  1020
273    D  G  D  V  T  F  F  G  A  L  K  L  L                     285
                         CD-XI

1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA  1080

1081 CCAAAAAAAAAAAAAAAAAA  1100
```

FIG. 1B

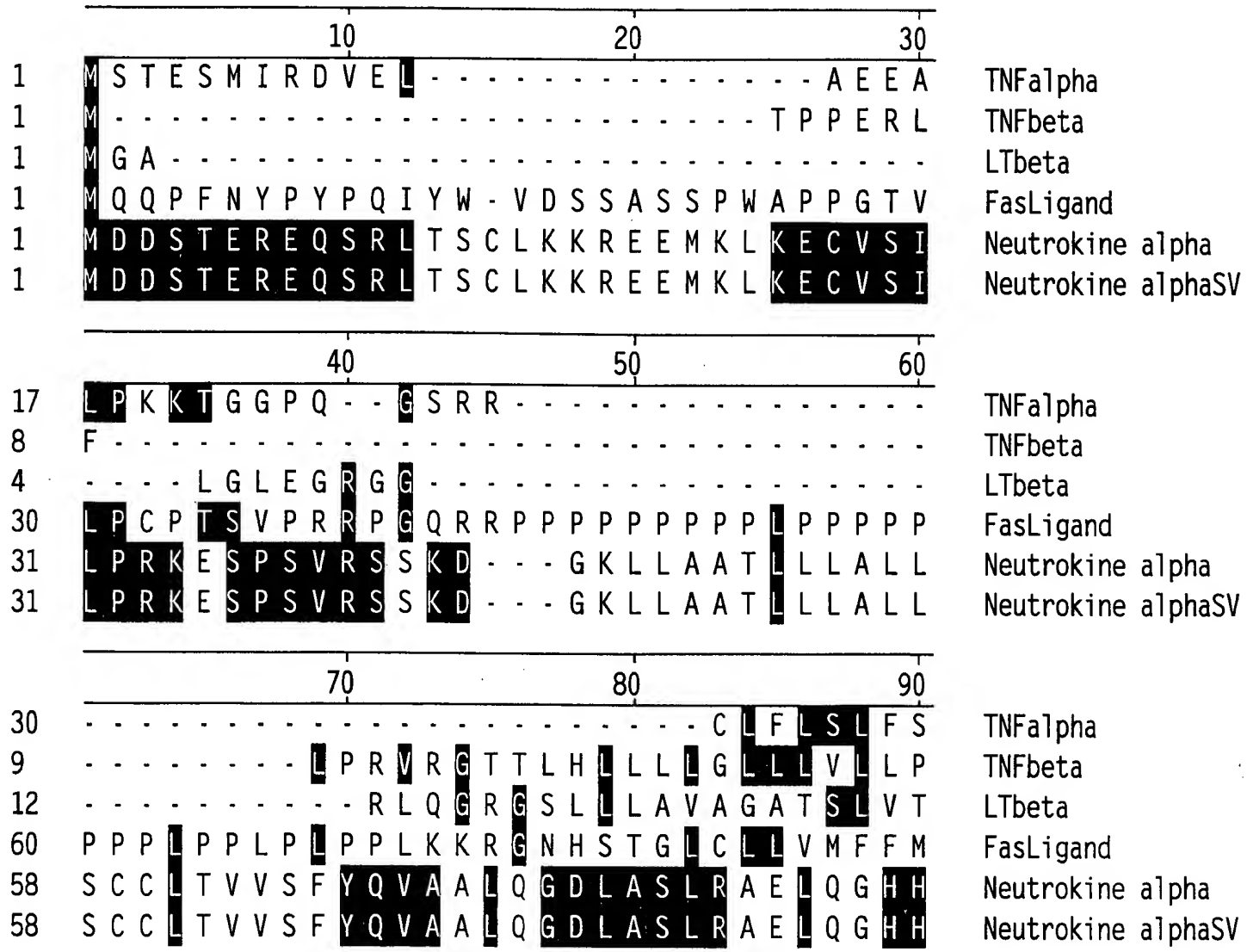
10 20 30
1 MSTESMIRDVEL----------AEEA TNFalpha
1 M----------TPPERL TNFbeta
1 MGA---------- LTbeta
1 MQQPFNYPYPQIYW-VDSSASSPWAPPGTV FasLigand
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alpha
1 MDDSTEREQSRLTSCLKKREEMKLKECVSI Neutrokine alphaSV
40 50 60
17 LPKKTGGPQ--GSRR---------- TNFalpha
8 F---------- TNFbeta
4 ----LGLEGRGG---------- LTbeta
30 LPCPTSVPRRPGQRRPPPPPPPPPLPPPPP FasLigand
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alpha
31 LPRKESPSVRSSKD---GKLLAATLLLALL Neutrokine alphaSV
70 80 90
30 ----------CLFLSLFS TNFalpha
9 ---------LPRVRGTTLHLLLLGLLLVLLP TNFbeta
12 ----------RLQGRGSLLLAVAGATSLVT LTbeta
60 PPPLPPLPLPPLKKRGNHSTGLCLLVMFFM FasLigand
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alpha
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH Neutrokine alphaSV

FIG.2A

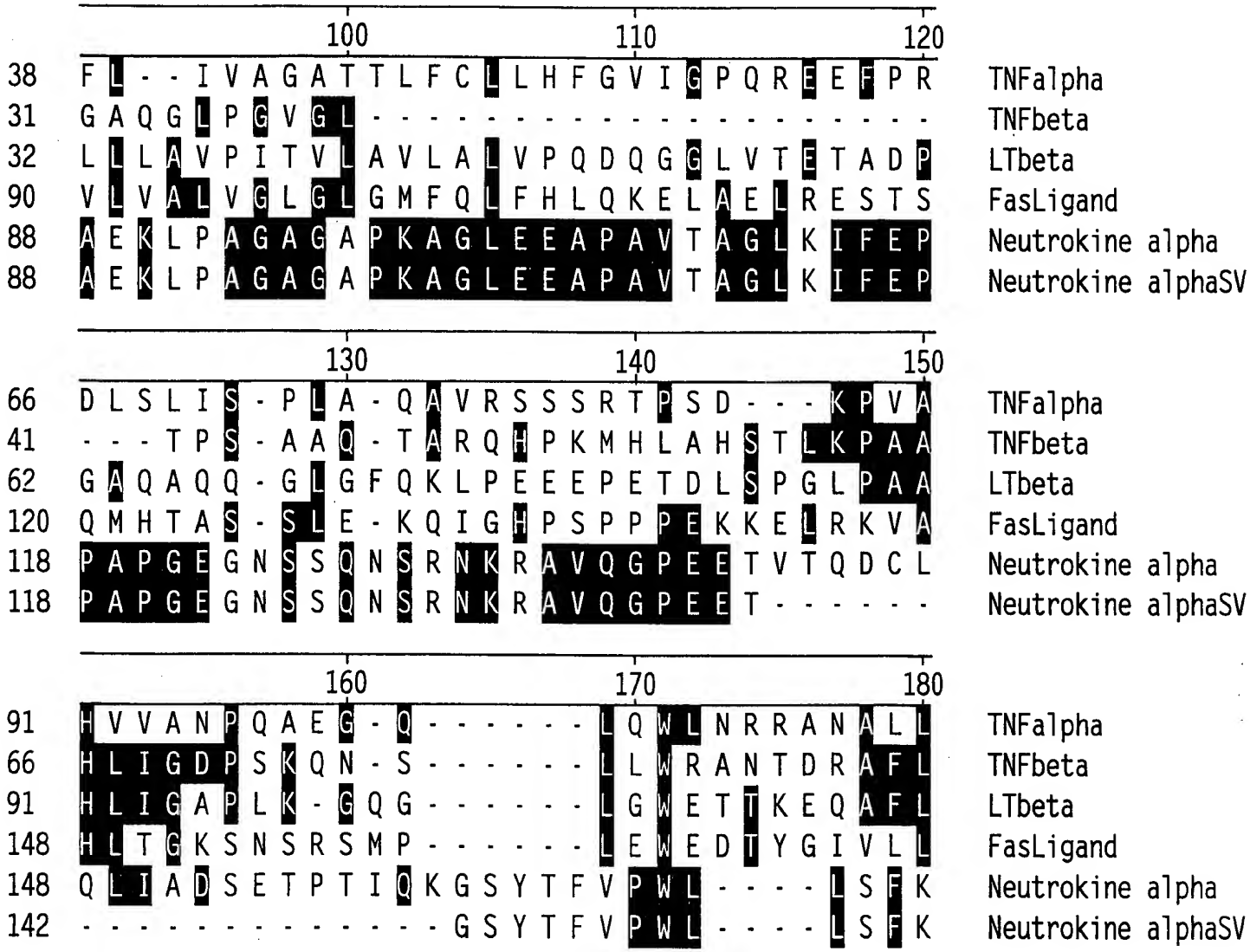
100 110 120
38 FL--IVAGATTLFCLLHFGVIGPQREEFPR TNFalpha
31 GAQGLPGVGL---------- TNFbeta
32 LLLAVPITVLAVLALVPQDQGGLVTETADP LTbeta
90 VLVALVGLGLGMFQLFHLQKELAELRESTS FasLigand
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alpha
88 AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP Neutrokine alphaSV
130 140 150
66 DLSLIS-PLA-QAVRSSSRTPSD---KPVA TNFalpha
41 ---TPS-AAQ-TARQHPKMHLAHSTLKPAA TNFbeta
62 GAQAQQ-GLGFQKLPEEEPETDLSPGLPAA LTbeta
120 QMHTAS-SLE-KQIGHPSPPPEKKELRKVA FasLigand
118 PAPGEGNSSQNSRNKRAVQGPEETVTQDCL Neutrokine alpha
118 PAPGEGNSSQNSRNKRAVQGPEET------ Neutrokine alphaSV
160 170 180
91 HVVANPQAEG-Q------LQWLNRRANALL TNFalpha
66 HLIGDPSKQN-S------LLWRANTDRAFL TNFbeta
91 HLIGAPLK-GQG------LGWETTKEQAFL LTbeta
148 HLTGKSNSRSMP------LEWEDTYGIVLL FasLigand
148 QLIADSETPTIQKGSYTFVPWL----LSFK Neutrokine alpha
142 ----------GSYTFVPWL----LSFK Neutrokine alphaSV

FIG.2B

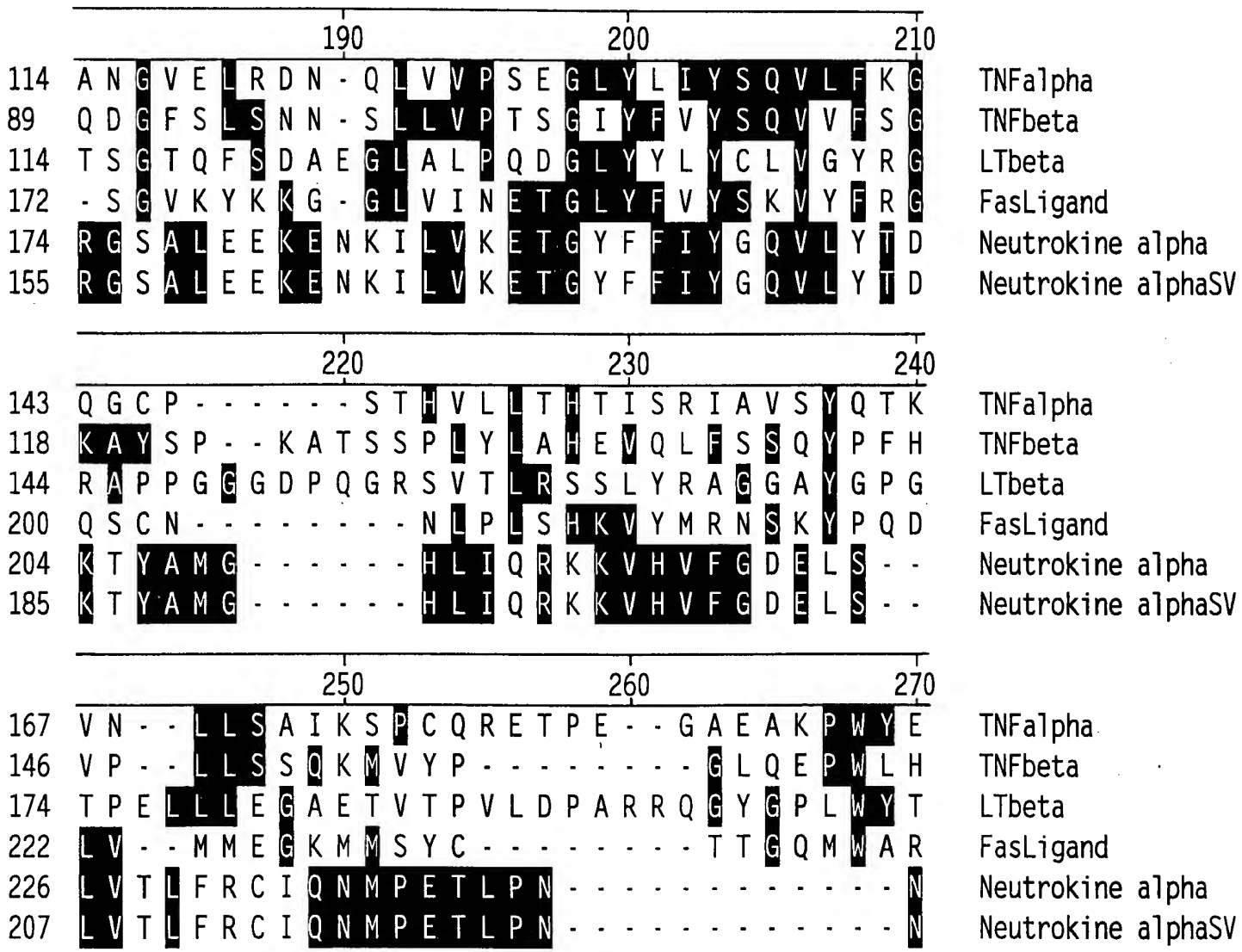
190
200
210
114 A N G V E L R D N - Q L V V P S E G L Y L I Y S Q V L F K G TNFalpha
89 Q D G F S L S N N - S L L V P T S G I Y F V Y S Q V V F S G TNFbeta
114 T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L V G Y R G LTbeta
172 - S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G FasLigand
174 R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D Neutrokine alpha
155 R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D Neutrokine alphaSV
220
230
240
143 Q G C P - - - - - - S T H V L L T H T I S R I A V S Y Q T K TNFalpha
118 K A Y S P - - K A T S S P L Y L A H E V Q L F S S Q Y P F H TNFbeta
144 R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G LTbeta
200 Q S C N - - - - - - - - N L P L S H K V Y M R N S K Y P Q D FasLigand
204 K T Y A M G - - - - - - H L I Q R K K V H V F G D E L S - - Neutrokine alpha
185 K T Y A M G - - - - - - H L I Q R K K V H V F G D E L S - - Neutrokine alphaSV
250
260
270
167 V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E TNFalpha
146 V P - - L L S S Q K M V Y P - - - - - - - - G L Q E P W L H TNFbeta
174 T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T LTbeta
222 L V - - M M E G K M M S Y C - - - - - - - - T T G Q M W A R FasLigand
226 L V T L F R C I Q N M P E T L P N - - - - - - - - - - - - N Neutrokine alpha
207 L V T L F R C I Q N M P E T L P N - - - - - - - - - - - - N Neutrokine alphaSV

FIG.2C

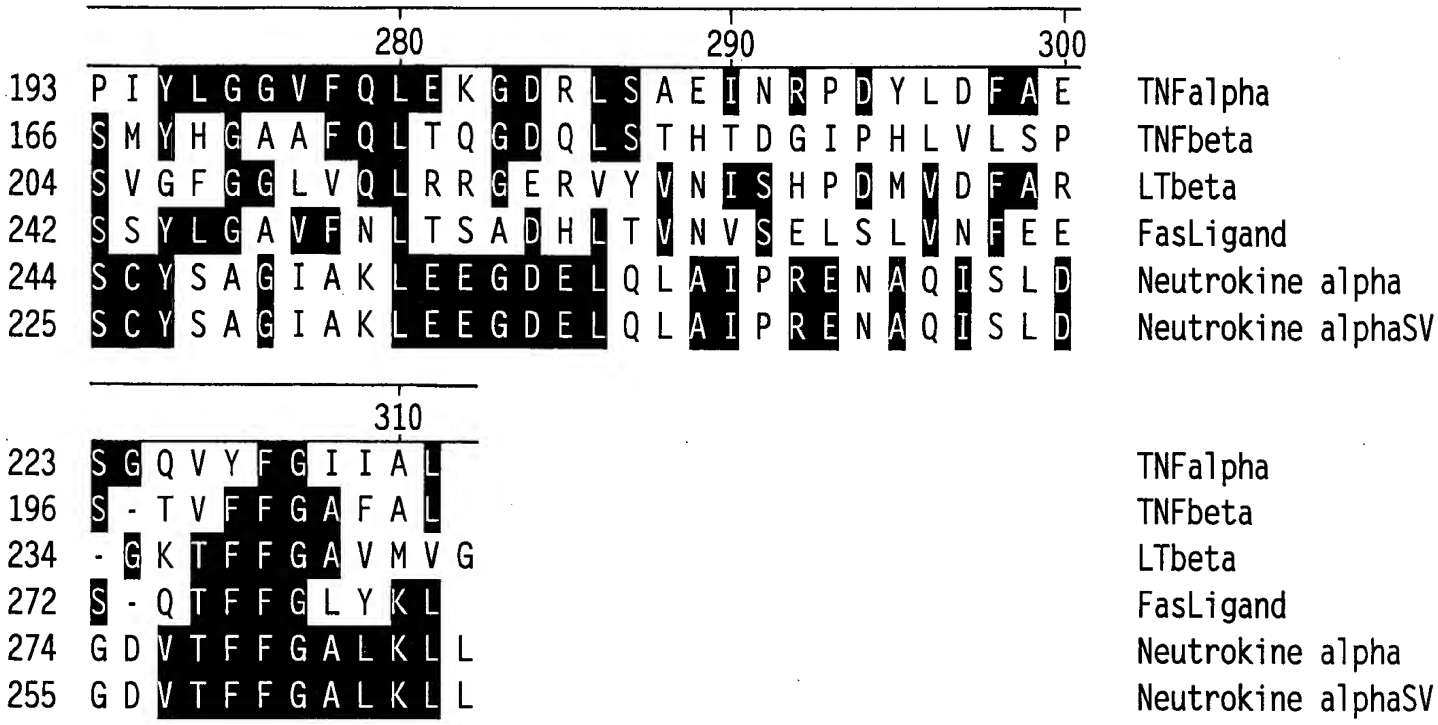
280
290
300
193 P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E TNFalpha
166 S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P TNFbeta
204 S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R LTbeta
242 S S Y L G A V F N L T S A D H L T V N V S E L S L V N F E E FasLigand
244 S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D Neutrokine alpha
225 S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D Neutrokine alphaSV
310
223 S G Q V Y F G I I A L TNFalpha
196 S - T V F F G A F A L TNFbeta
234 - G K T F F G A V M V G LTbeta
272 S - Q T F F G L Y K L FasLigand
274 G D V T F F G A L K L L Neutrokine alpha
255 G D V T F F G A L K L L Neutrokine alphaSV

FIG.2D

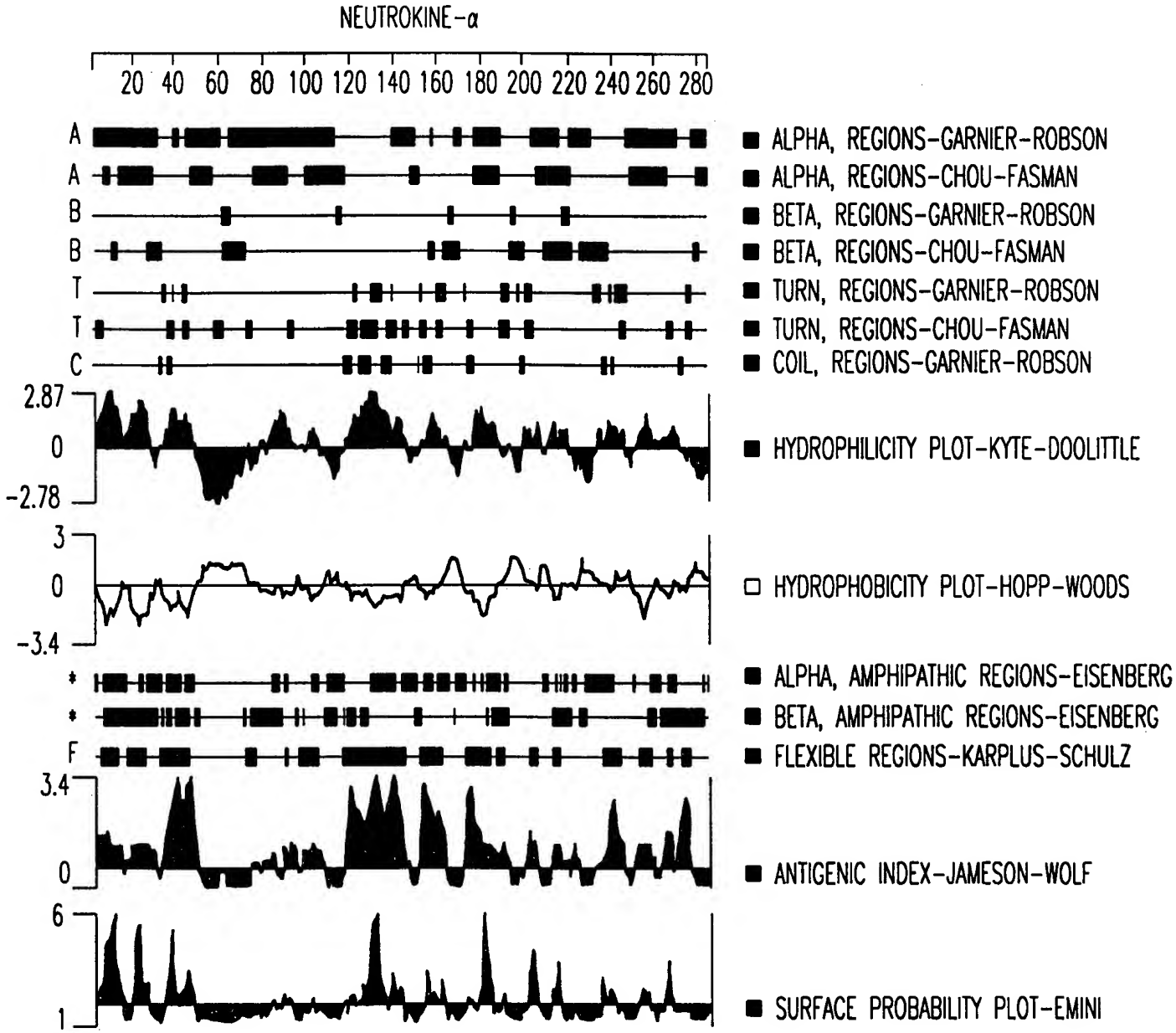
NEUTROKINE-α
20 40 60 80 100 120 140 160 180 200 220 240 260 280
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
2.87
0
-2.78
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI

FIG.3

```
                1                                                  50
HSOAD55R  .........A GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HNEDU15X  ...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HSLAH84R  .AATTCGGCA NAGNAAACTG GTTACTTTTT TATATATGGT CAGGTTTTAT
HLTBM08R  AATTCGGCAC GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCACCGCG

               51                                                 100
HSOAD55R  GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTC
HNEDU15X  GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTC
HSLAH84R  ATACTGATAA GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC
HLTBM08R  GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA

              101                                                 150
HSOAD55R  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HNEDU15X  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HSLAH84R  CATGTCTTTG GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA
HLTBM08R  GAACAGCAGA AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC

              151                                                 200
HSOAD55R  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HNEDU15X  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HSLAH84R  AAATATGCCT GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG
HLTBM08R  AAGACTGCTT GCAACTGNTT GCAGACAGTG AAACACCAAC TATACAAAAA

              201                                                 250
HSOAD55R  AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG
HNEDU15X  AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG
HSLAH84R  CAAAACTGGN AGGAAGGA.. ...GATGAAC TCCAACTTGC AATACCAGGG
HLTBM08R  GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG

              251                                                 300
HSOAD55R  GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HNEDU15X  GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HSLAH84R  GAAAATGCAC AATTATCACT GGGATGGAGA TGTTCACATT TTTTGGGTGC
HLTBM08R  TCTGGAAACA TTTTGCCAAA CTCTTCAGAT ACTCTTTNCT CTCTGGGAAT

              301                                                 350
HSOAD55R  CAACCTTGNT GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTTNTT.
HNEDU15X  CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCTTTC
HSLAH84R  CATTGAAACT GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTTNC
HLTBM08R  CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT

              351                                                 400
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TACCAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT
HSLAH84R  CTNCCTNTTC TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA
HLTBM08R  AAGTTTTAAA AGGGGAGTGC CCTTAGGAGG AAAAGGGGAT AAATATTGGC
```

FIG.4A

```
            401                                                 450
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    GCAGGGCCAC CACGCGGAGA AGCTGCCAGC AGGAGCAGGA GCCCCCAAGG
HSLAH84R    ATAACCCAAA AAAANNTTAA ANGGGTANGN GNNANANGNG GGGNNGTTNN
HLTBM08R    CAAGGNACTG GTTANTTTNT AAATATGGTC AGGTTTNTAT ANCTGGTAGG

            451                                                 500
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCGGCCTGGA GGAAGCTCCA GCTGTCACCG CGGGACTGAA AATCTTTGAA
HSLAH84R    CNNGNNGNNT TTTNGGNNTA TNTTNTNNTN GGGNNNNGTA AAAATGGGGC
HLTBM08R    CCTCGCCATG GGCATTNATT CANGGNGAGG NCNNTCTTTT GGGNTGA...

            501                                                 550
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCACCAGCTC CAGGAGAAGG CAACTCCAGT CAGAACAGCA GAAATAAGCG
HSLAH84R    CNANGGGGGN TTTTT..... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            551                                                 600
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TGCCGTTCAG GGTCCAGAAG AAACAGTCAC TCAAGACTGC TTGCAACTGA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            601                                                 650
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TTGCAGACAG TGAAACACCA ACTATACAAA AAGGATCTTA CACATTTGTT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            651                                                 700
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCATGGCTTC TCAGCTTTAA AAGGGGAAGT GCCCTAGAAG AAAAAGAGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            701                                                 750
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TAAAATATTG GTCAAAGAAA CTGGTTACTT TTTTATATAT GGTCAGGTTT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            751                                                 800
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TATATACTGA TAAGACCTAC GCCATGGGAC ATCTAATTCA GAGGAAGAAG
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........
```

FIG.4B

```
                801                                                 850
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  GTCCATGTCT TTGGGGATGA ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

                851                                                 900
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TCAAAATATG CCTGAAACAC TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

                901                                                 950
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  TTGCAAAACT GGAAGAAGGA GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

                951                                                1000
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  AATGCACAAA TATCACTGGA TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

               1001                                                1050
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  ACTGCTGTGA CCTACTTACA CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

               1051                                                1100
HSOAD55R  .......... .......... .......... .......... ..........
HNEDU15X  CTGTACCTCT AAGAAGAAAG AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R  .......... .......... .......... .......... ..........
HLTBM08R  .......... .......... .......... .......... ..........

               1101
HSOAD55R  ......
HNEDU15X  AAAAAA
HSLAH84R  ......
HLTBM08R  ......
```

FIG.4C

Neutrokine-αSV

```
   1  ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA   60
   1  M  D  D  S  T  E  R  E  Q  S  R  L  T  S  C  L  K  K  R  E    20

  61  GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGA  120
  21  E  M  K  L  K  E  C  V  S  I  L  P  R  K  E  S  P  S  V  R    40
                                                 CD-I

 121  TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC  180
  41  S  S  K  D  G  K  L  L  A  A  T  L  L  L  A  L  L  S  C  C    60
         CD-I

 181  CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG  240
  61  L  T  V  V  S  F  Y  Q  V  A  A  L  Q  G  D  L  A  S  L  R    80
                                              CD-II

 241  GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCCAAGGCC  300
  81  A  E  L  Q  G  H  H  A  E  K  L  P  A  G  A  G  A  P  K  A   100
      CD-II                                      CD-III

 301  GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA  360
 101  G  L  E  E  A  P  A  V  T  A  G  L  K  I  F  E  P  P  A  P   120
    CD-III
              #
 361  GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAGGGTCCAGAAGAA  420
 121  G  E  G  N  S  S  Q  N  S  R  N  K  R  A  V  Q  G  P  E  E   140

 421  ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA  480
 141  T  G  S  Y  T  F  V  P  W  L  L  S  F  K  R  G  S  A  L  E   160
                                              CD-IV

 481  GAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTTATATATGGTCAGGTT  540
 161  E  K  E  N  K  I  L  V  K  E  T  G  Y  F  F  I  Y  G  Q  V   180
      CD-IV                                  CD-V

 541  TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC  600
 181  L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q  R  K  K  V  H  V   200
               CD-VI                          CD-VII
```

FIG.5A

Neutrokine-αSV

```
601  TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA  660
201  F  G  D  E  L  S  L  V  T  L  F  R  C  I  Q  N  M  P  E  T   220
     CD-VIII                       CD-VIII

661  CTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC  720
221  L  P  N  N  S  C  Y  S  A  G  I  A  K  L  E  E  G  D  E  L   240
                  CD-IX                          CD-X

721  CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT  780
241  Q  L  A  I  P  R  E  N  A  Q  I  S  L  D  G  D  V  T  F  F   260
        CD-X                                                CD-XI

781  GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC  840
261  G  A  L  K  L  L                                            266
        CD-XI

841  TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAA  900

901  AAA  903
```

FIG.5B

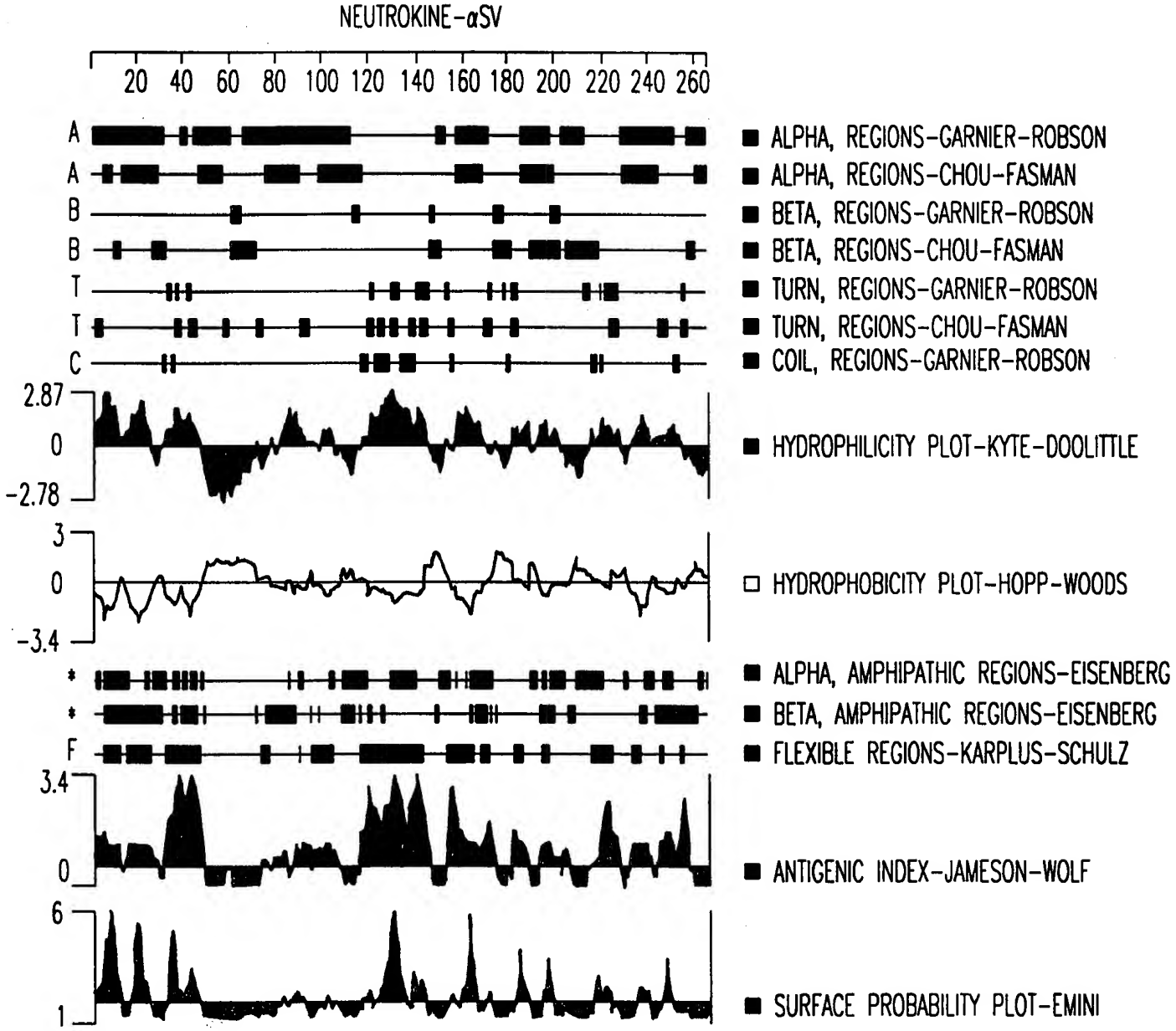

FIG.6

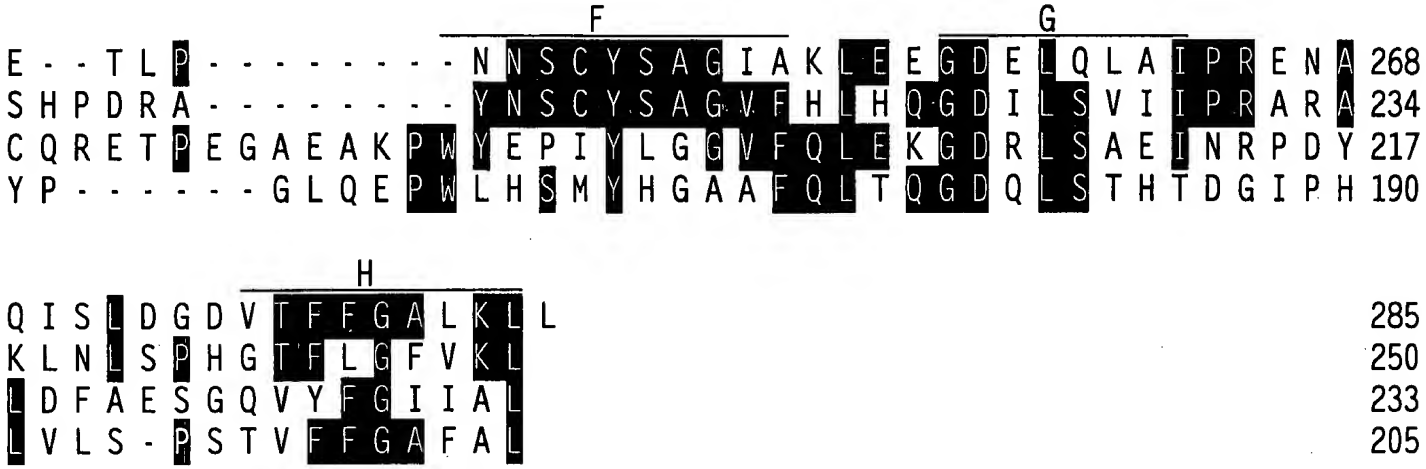

FIG.7A-2

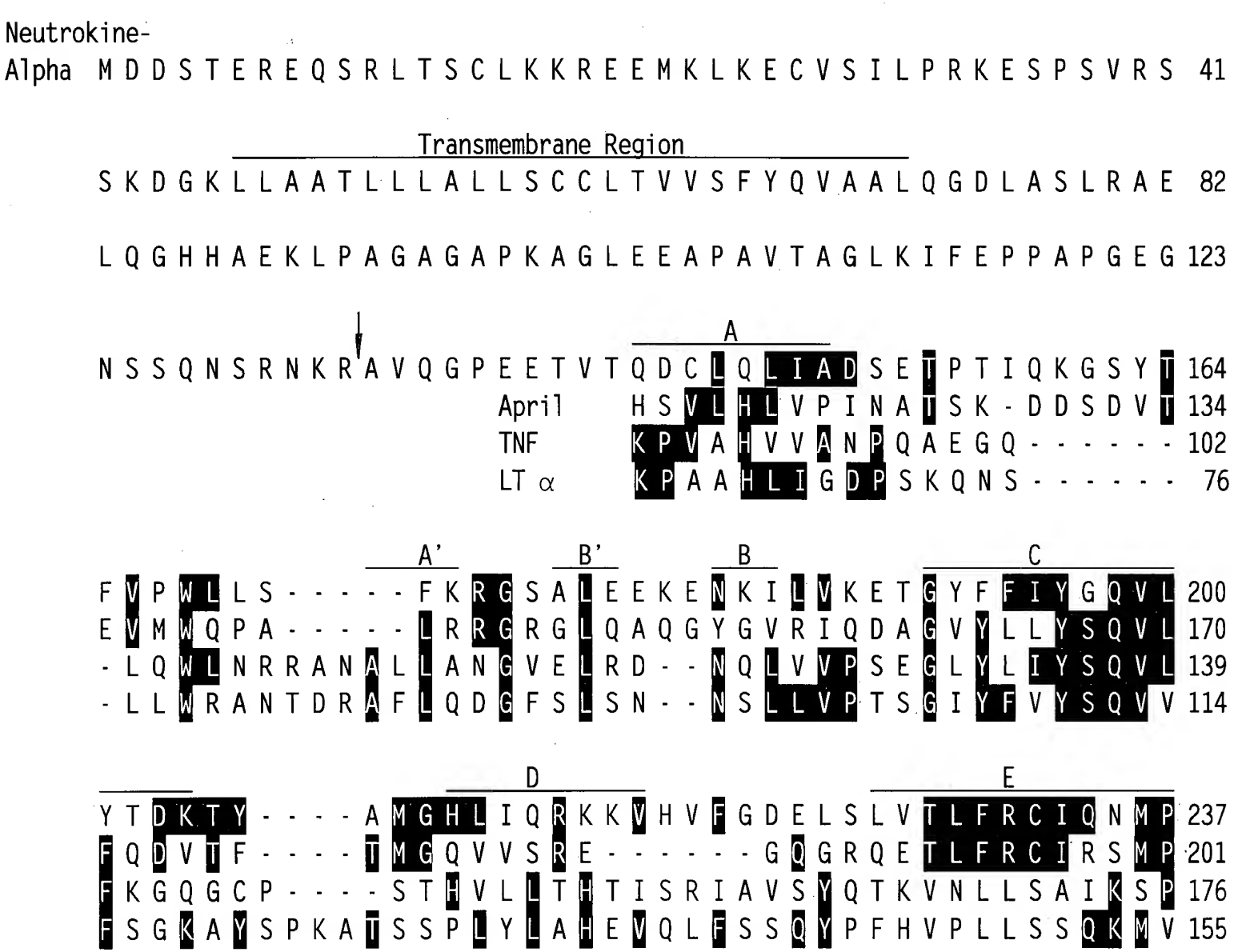

FIG.7A-1

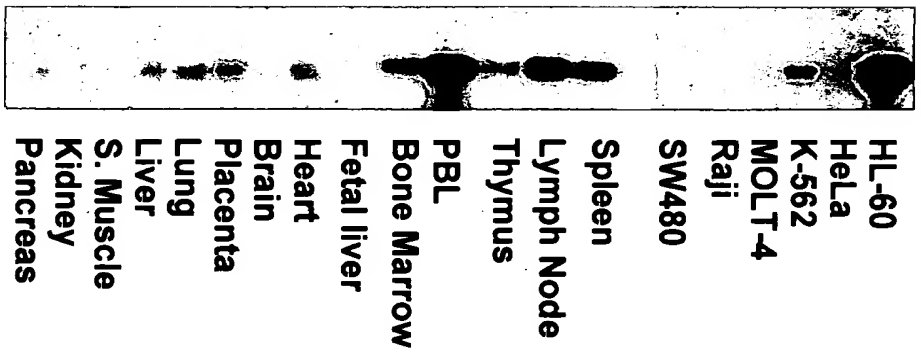

FIG.7B

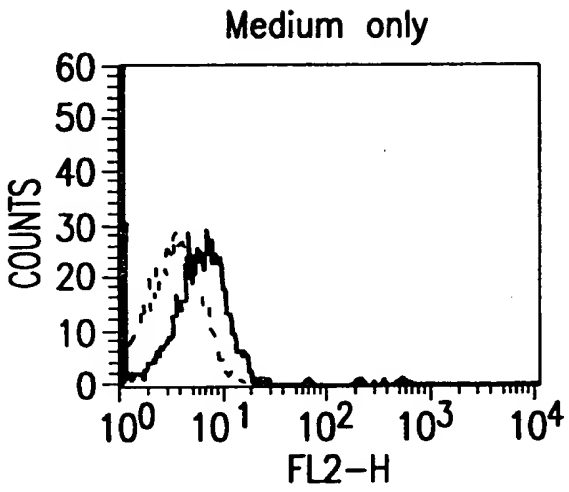

FIG.8A

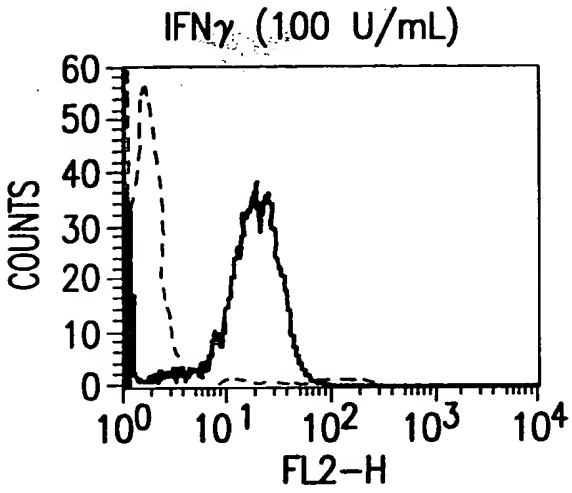

FIG.8B

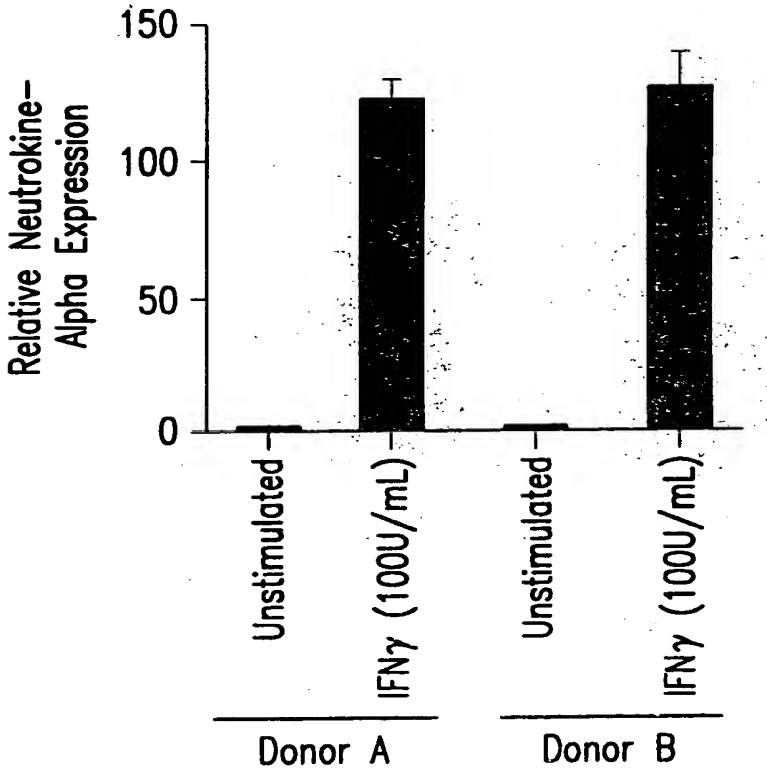

FIG.8C

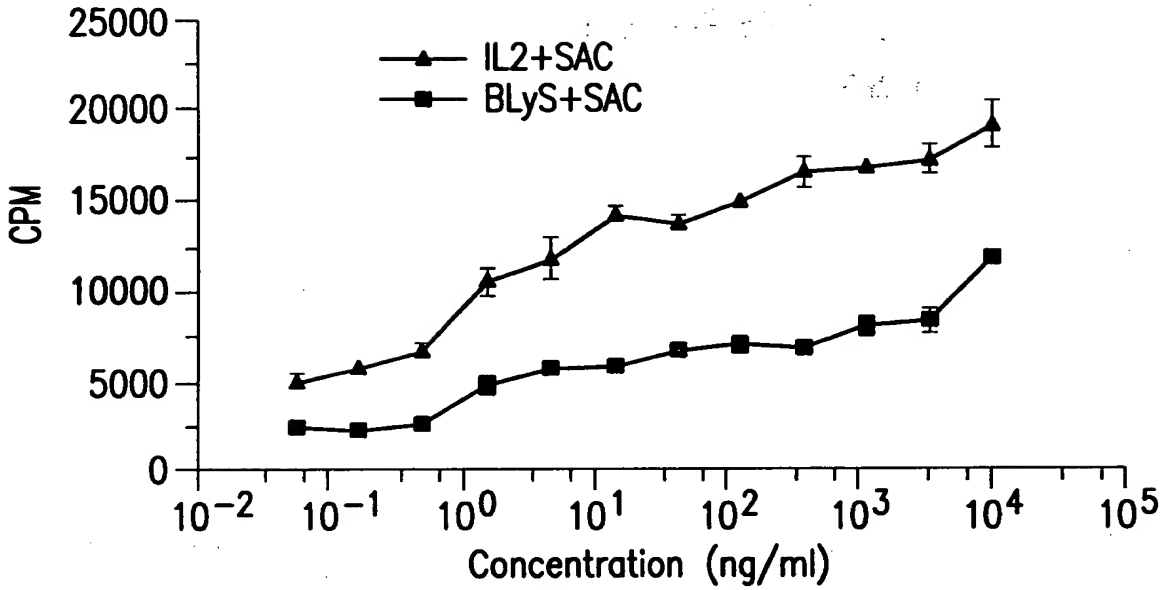

FIG. 9A

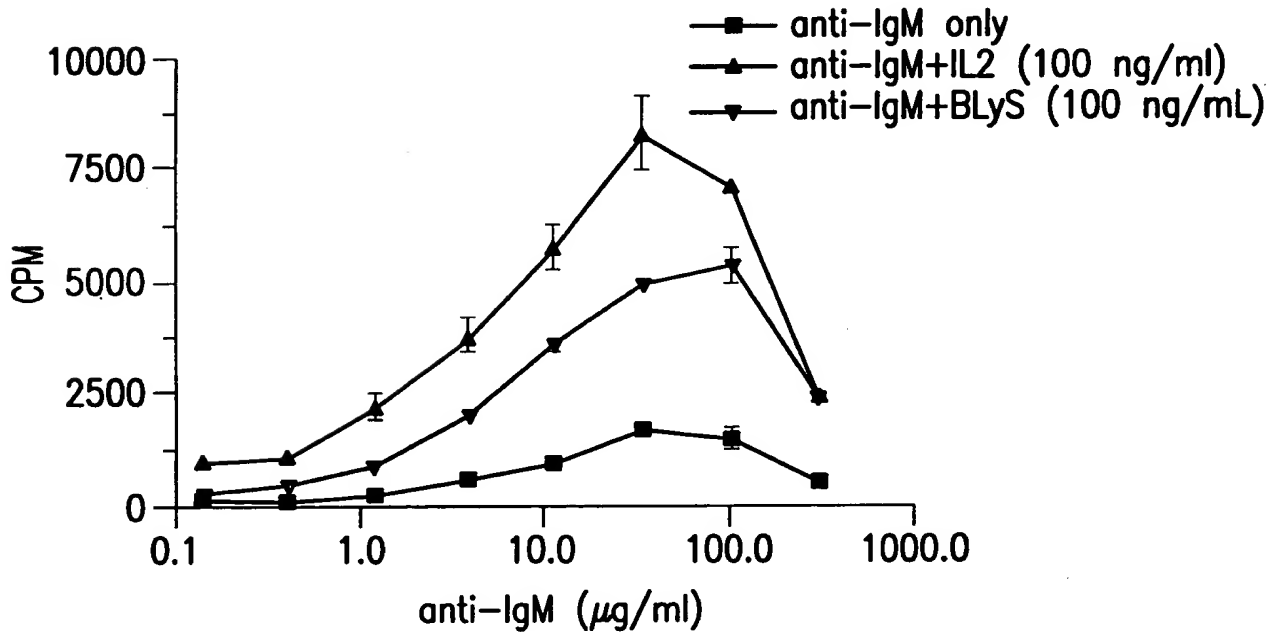

FIG. 9B

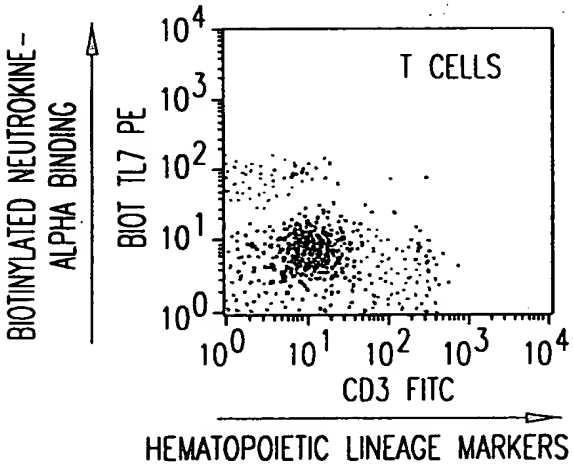

FIG.10A

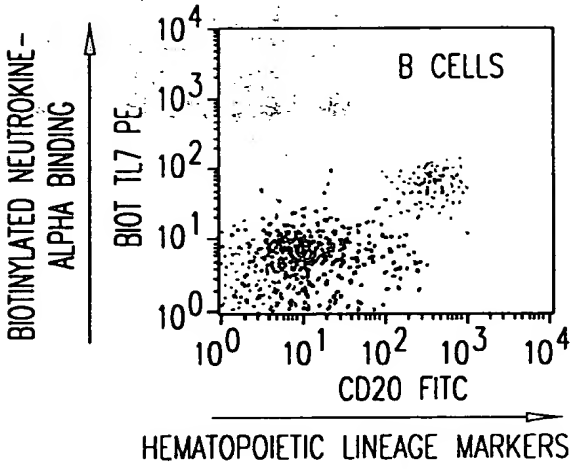

FIG.10B

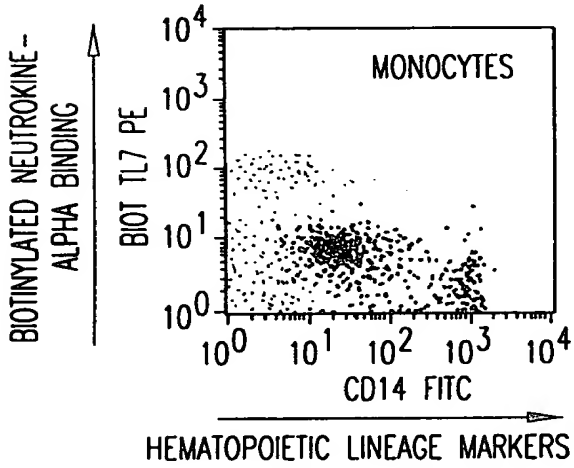

FIG.10C

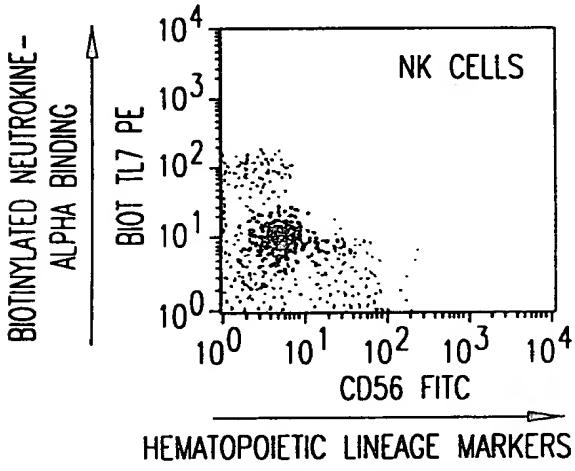

FIG.10D

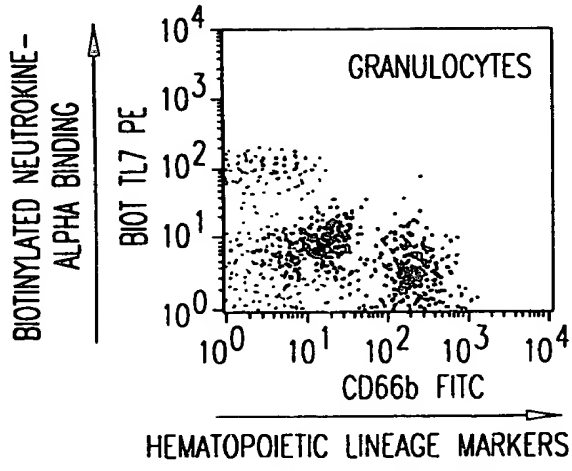

FIG.10E

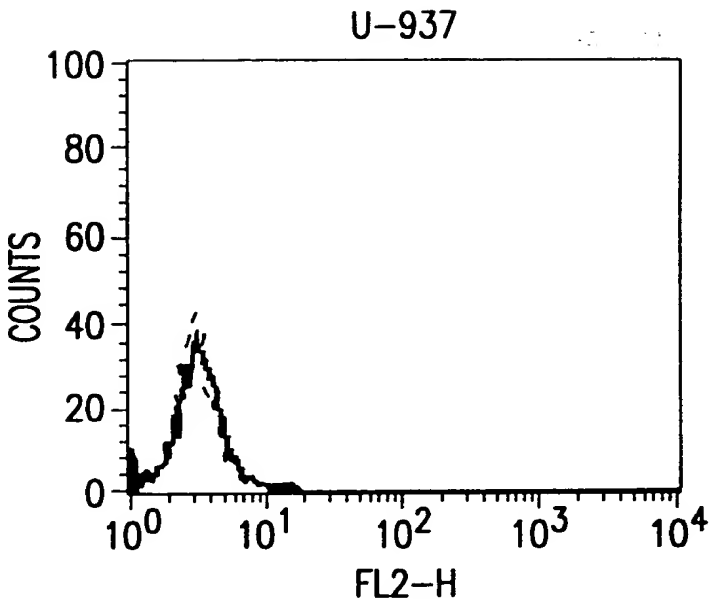

FIG.10F

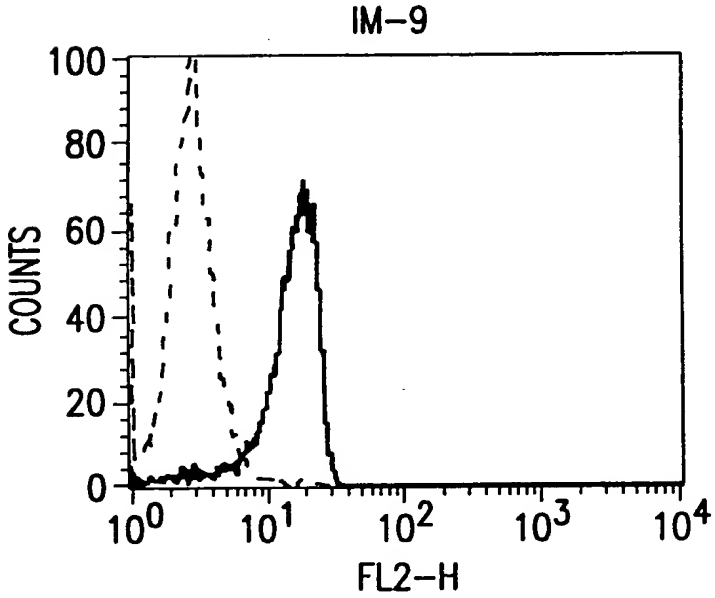

FIG.10G

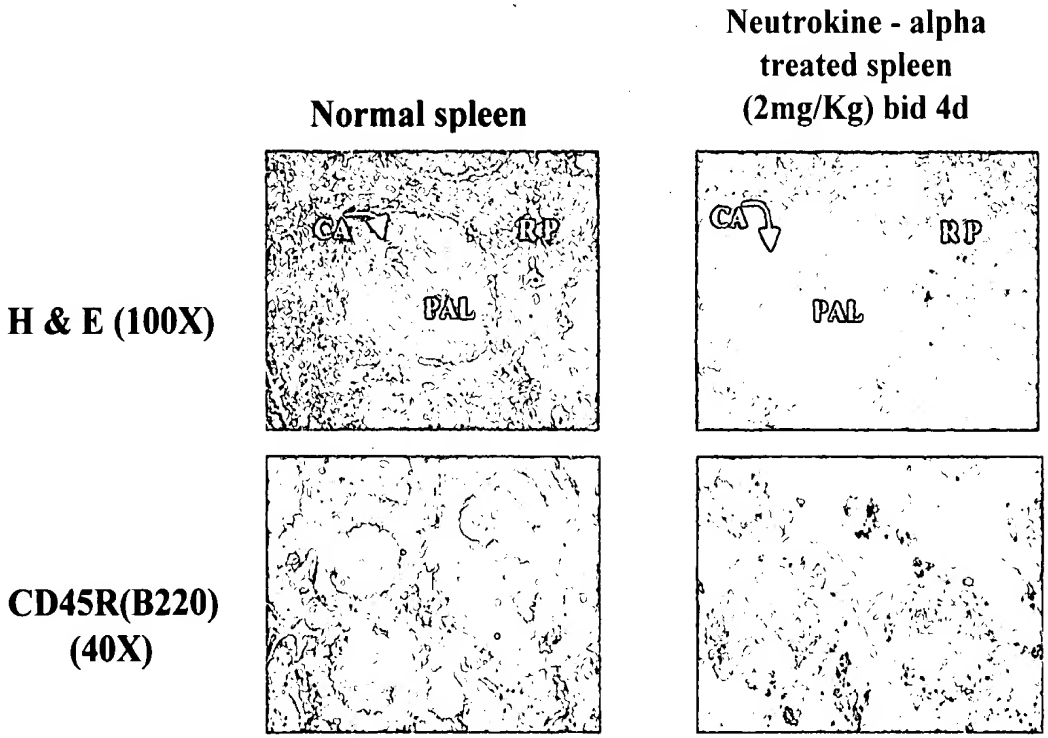

FIG.11A

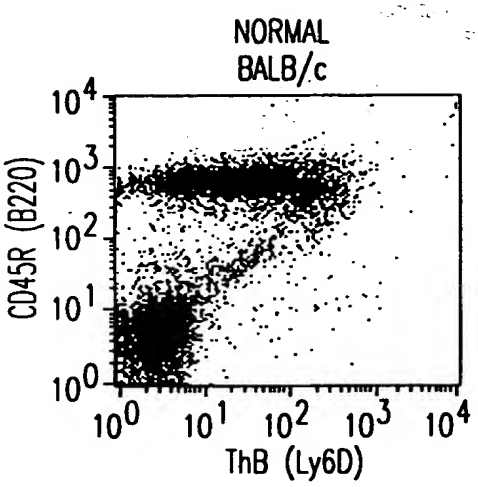

FIG. 11B

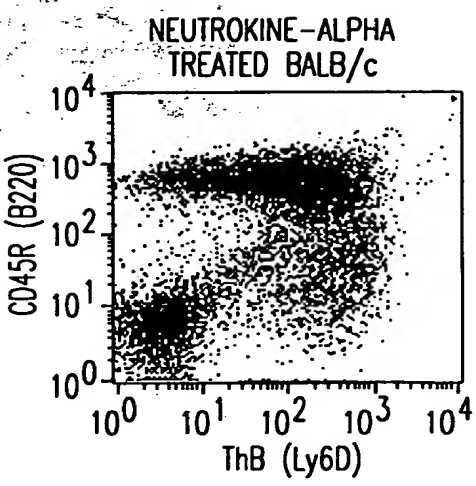

FIG. 11C

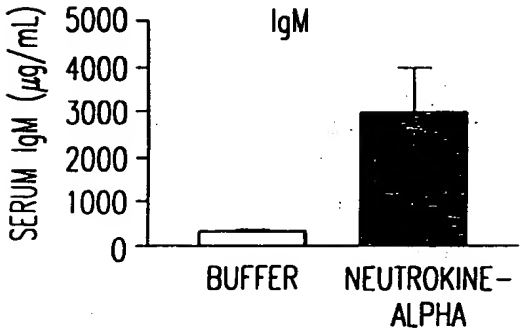

FIG. 11D

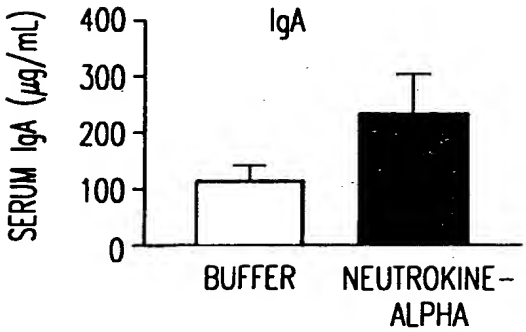

FIG. 11E

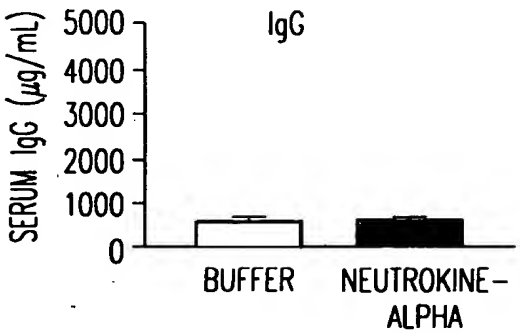

FIG. 11F